

1

SEQUENCE LISTING

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<140> 09/853,033

<141> 2001-05-11

<150> FR 00/12570

<151> 2000-10-03

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<170> PatentIn Ver. 2.1

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- gcg gcc gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc ccc tac
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 Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
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His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met 520 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 565 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro 585 Ala Thr Val 595 <210> 3 <211> 1983 <212> DNA <213> Artificial sequence <220> <221> CDS <222> (1)..(1983) <223> Description of Artificial Sequence: Chimeric sequence Homosapiens-Bacteriophage P1 atg tcc aat tta ctg acc gta cac caa aat ttg cct gca tta ccg gtc Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val 1 gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg 25 gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe 50 ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg 240 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn 85

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				aat Asn 245												768
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Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
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Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu 165 170 175

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Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp 210 215 220

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Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu 245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val 325 330 335

Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg 340 345 350

Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys 355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu 370 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg 385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 405 410 415

Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 420 425 430

Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp 435 440 445

Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 450 455 460

Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly 465 470 475 480

Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485 490 495

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Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser 515 520 525

Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530 540

Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545 550 555 560

Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565 570 575

Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser 580 585 590

Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Met 595 600 605

Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser 610 620

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Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe 645 650 655

Pro Ala Thr Val 660

<210> 5

<211> 1983

<212> DNA

<213> Artificial sequence <220> <221> CDS <222> (1)..(1983) <220> <223> Description of Artificial Sequence: Chimeric sequence Homosapiens-Bacteriophage P1 <400> 5 atg tcc aat tta ctg acc gta cac caa aat ttg cct gca tta ccg gtc Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg 96 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val 40 tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg 240 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn 85 atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala 100 105 gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly 115 gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag 432 Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln 130 gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat 480 Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn 145 150 ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa 528 Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu 165 att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg

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gtc Val	atg Met	aac Asn	tat Tyr	atc Ile 325	cgt Arg	aac Asn	ctg Leu	gat Asp	agt Ser 330	gaa Glu	aca Thr	ggg Gly	gca Ala	atg Met 335	gtg Val	1008
cgc Arg	ctg Leu	ctg Leu	gaa Glu 340	gat Asp	ggc Gly	gat Asp	ctc Leu	gag Glu 345	cca Pro	tct Ser	gct Ala	gga Gly	gac Asp 350	atg Met	aga Arg	1056
gct Ala	gcc Ala	aac Asn 355	ctt Leu	tgg Trp	cca Pro	agc Ser	ccg Pro 360	ctc Leu	atg Met	atc Ile	aaa Lys	cgc Arg 365	tct Ser	aag Lys	aag Lys	1104
aac Asn	agc Ser 370	ctg Leu	gcc Ala	ttg Leu	tcc Ser	ctg Leu 375	acg Thr	gcc Ala	gac Asp	cag Gln	atg Met 380	gtc Val	agt Ser	gcc Ala	ttg Leu	1152
ttg Leu 385	gat Asp	gct Ala	gag Glu	ccc Pro	ccc Pro 390	ata Ile	ctc Leu	tat Tyr	tcc Ser	gag Glu 395	tat Tyr	gat Asp	cct Pro	acc Thr	aga Arg 400	1200
ccc Pro	ttc Phe	agt Ser	gaa Glu	gct Ala 405	tcg Ser	atg Met	atg Met	ggc Gly	tta Leu 410	ctg Leu	acc Thr	aac Asn	ctg Leu	gca Ala 415	gac Asp	1248

agg Arg	gag Glu	g cto ı Lei	g gt u Va 42	T UI	c ato s Mei	g ato	c aad Asi	c tgg n Trj 42!	p Al	g aa a Ly	g ag	g gto g Va]	g cca L Pro 430	o Gl	c ttt y Phe	1296
gtg Val	gat Asp	tto Lei 435	1 111	c cto	c cat u His	gat S Asp	Cag Gli 440	ı Val	cae l Hi	c cti s Lei	t cta u Lei	a gaa u Glu 445	г Суя	gc Ala	c tgg a Trp	1344
cta Leu	gag Glu 450	тте	cto Lei	g ato 1 Met	g att Ile	ggt Gl _y 455	. Lei	gto Val	c tgg	g cgo	g Sei 460	r Met	gag Glu	g cad His	c cca s Pro	1392
gtg Val 465	aag Lys	cta Leu	ctg Lei	g ttt 1 Phe	gct Ala 470	Pro	aac Asr	ttg Leu	g cto Lei	tto Lei 475	ı Asp	agg Arg	aac Asn	caç Glr	g gga n Gly 480	1440
aaa Lys	tgt Cys	gta Val	gag Glu	ggo Gly 485	Met	gtg Val	gag Glu	ato Ile	tto Phe	Asp	ato Met	g ctg : Leu	ctg Leu	gct Ala 495	aca Thr	1488
tca Ser	tct Ser	cgg Arg	Phe	Arg	atg Met	atg Met	aat Asn	ctg Leu 505	Gln	gga Gly	gag Glu	g gag Glu	ttt Phe 510	gtg Val	tgc Cys	1536
ctc Leu	aaa Lys	tct Ser 515	att Ile	att Ile	ttg Leu	ctt Leu	aat Asn 520	tct Ser	gga Gly	gtg Val	tac Tyr	aca Thr 525	ttt Phe	ctg Leu	tcc Ser	1584
261	acc Thr 530	ctg Leu	aag Lys	tct Ser	ctg Leu	gaa Glu 535	gag Glu	aag Lys	gac Asp	cat His	atc Ile 540	cac His	cga Arg	gtc Val	ctg Leu	1632
gac a Asp 1 545	aag Lys	atc Ile	aca Thr	gac Asp	act Thr 550	ttg Leu	atc Ile	cac His	ctg Leu	atg Met 555	gcc Ala	aag Lys	gca Ala	ggc Gly	ctg Leu 560	1680
acc o	ctg Leu	cag Gln	cag Gln	cag Gln 565	cac His	cag Gln	cgg Arg	ctg Leu	gcc Ala 570	cag Gln	ctc Leu	ctc Leu	ctc Leu	atc Ile 575	ctc Leu	1728
tcc c Ser H	cac His	atc Ile	agg Arg 580	cac His	atg Met	agt Ser	aac Asn	aaa Lys 585	ggc Gly	atg Met	gag Glu	cat His	ctg Leu 590	tac Tyr	agc Ser	1776
atg a Met I	yys '	tgc Cys 595	aag Lys	aac Asn	gtg Val	gtg Val	ccc Pro 600	ctc Leu	tat Tyr	gac Asp	ctg Leu	ctg Leu 605	ctg Leu	gag Glu	gcg Ala	1824
gcg g Ala A	sp i	gcc Ala	cac His	cgc Arg	ьеи	cat His 615	gcg Ala	ccc Pro	act Thr	agc Ser	cgt Arg 620	gga Gly	gly ggg	gca Ala	tcc Ser	1872
gtg g Val G 625	ag d	gag Glu	acg Thr	Asp	caa Gln 630	agc Ser	cac His	ttg Leu	gcc Ala	act Thr 635	gcg Ala	ggc Gly	tct Ser	act Thr	tca Ser 640	1920

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Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe 645

cct gcc aca gct tga
Pro Ala Thr Ala 660

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<212> PRT
<213> Artificial sequence

<223> Description of Artificial Sequence: Chimeric sequence Homosapiens-Bacteriophage P1

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Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe 50 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln 130 135 140

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp 215 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys 230 235 Arg Val Arg Lys Asn Gly Val Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile 265 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile 310 315 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val 330 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys 360 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 405 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 425 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 455 Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly 470 475 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys 505

Leu	Lys	Ser 515	Ile	Ile	Leu	Leu	Asn 520	Ser	Gly	Val	Tyr	Thr 525	Phe	Leu	Ser	
Ser	Thr 530	Leu	Lys	Ser	Leu	Glu 535	Glu	Lys	Asp	His	Ile 540	His	Arg	Val	Leu	
Asp 545		Ile	Thr	Asp	Thr 550	Leu	Ile	His	Leu	Met 555	Ala	Lys	Ala	Gly	Leu 560	
Thr	Leu	Gln	Gln	Gln 565	His	Gln	Arg	Leu	Ala 570	Gln	Leu	Leu	Leu	Ile 575	Leu	
Ser	His	Ile	Arg 580	His	Met	Ser	Asn	Lys 585	Gly	Met	Glu	His	Leu 590	Tyr	Ser	
Met	Lys	Cys 595	Lys	Asn	Val	Val	Pro 600	Leu	Tyr	Asp	Leu	Leu 605	Leu	Glu	Ala	
Ala	Asp 610	Ala	His	Arg	Leu	His 615	Ala	Pro	Thr	Ser	Arg 620	Gly	Gly	Ala	Ser	
Val 625	Glu	Glu	Thr	Asp	Gln 630	Ser	His	Leu	Ala	Thr 635	Ala	Gly	Ser	Thr	Ser 640	
Ser	His	Ser	Leu	Gln 645	Lys	Tyr	Tyr	Ile	Thr 650	Gly	Glu	Ala	Glu	Gly 655	Phe	
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gat Asp	gca Ala	acg Thr	agt Ser 20	gat Asp	gag Glu	gtt Val	cgc Arg	aag Lys 25	aac Asn	ctg Leu	atg Met	gac Asp	atg Met 30	ttc Phe	agg Arg	96
gat Asp	cgc Arg	cag Gln 35	gcg Ala	ttt Phe	tct Ser	gag Glu	cat His 40	acc Thr	tgg Trp	aaa Lys	atg Met	ctt Leu 45	ctg Leu	tcc Ser	gtt Val	144

tgc Cys	cgg Arg 50	tcg Ser	tgg Trp	gcg Ala	gca Ala	tgg Trp 55	tgc Cys	aag Lys	ttg Leu	aat Asn	aac Asn 60	cgg Arg	aaa Lys	tgg Trp	ttt Phe	192
ccc Pro 65	gca Ala	gaa Glu	cct Pro	gaa Glu	gat Asp 70	gtt Val	cgc Arg	gat Asp	tat Tyr	ctt Leu 75	cta Leu	tat Tyr	ctt Leu	cag Gln	gcg Ala 80	240
cgc Arg	ggt Gly	ctg Leu	gca Ala	gta Val 85	aaa Lys	act Thr	atc Ile	cag Gln	caa Gln 90	cat His	ttg Leu	ggc Gly	cag Gln	cta Leu 95	aac Asn	288
atg Met	ctt Leu	cat His	cgt Arg 100	cgg Arg	tcc Ser	Gly 999	ctg Leu	cca Pro 105	cga Arg	cca Pro	agt Ser	gac Asp	agc Ser 110	aat Asn	gct Ala	336
gtt Val	tca Ser	ctg Leu 115	gtt Val	atg Met	cgg Arg	cgg Arg	atc Ile 120	cga Arg	aaa Lys	gaa Glu	aac Asn	gtt Val 125	gat Asp	gcc Ala	ggt Gly	384
gaa Glu	cgt Arg 130	gca Ala	aaa Lys	cag Gln	gct Ala	cta Leu 135	gcg Ala	ttc Phe	gaa Glu	cgc Arg	act Thr 140	gat Asp	ttc Phe	gac Asp	cag Gln	432
gtt Val 145	cgt Arg	tca Ser	ctc Leu	atg Met	gaa Glu 150	aat Asn	agc Ser	gat Asp	cgc Arg	tgc Cys 155	cag Gln	gat Asp	ata Ile	cgt Arg	aat Asn 160	480
ctg Leu	gca Ala	ttt Phe	ctg Leu	999 Gly 165	att Ile	gct Ala	tat Tyr	aac Asn	acc Thr 170	ctg Leu	tta Leu	cgt Arg	ata Ile	gcc Ala 175	gaa Glu	528
att Ile	gcc Ala	agg Arg	atc Ile 180	agg Arg	gtt Val	aaa Lys	gat Asp	atc Ile 185	tca Ser	cgt Arg	act Thr	gac Asp	ggt Gly 190	gly ggg	aga Arg	576
atg Met	tta Leu	atc Ile 195	cat His	att Ile	ggc Gly	aga Arg	acg Thr 200	aaa Lys	acg Thr	ctg Leu	gtt Val	agc Ser 205	acc Thr	gca Ala	ggt Gly	624
gta Val	gag Glu 210	aag Lys	gca Ala	ctt Leu	agc Ser	ctg Leu 215	999 Gly	gta Val	act Thr	aaa Lys	ctg Leu 220	gtc Val	gag Glu	cga Arg	tgg Trp	672
att Ile 225	tcc Ser	gtc Val	tct Ser	ggt Gly	gta Val 230	gct Ala	gat Asp	gat Asp	ccg Pro	aat Asn 235	aac Asn	tac Tyr	ctg Leu	ttt Phe	tgc Cys 240	720
cgg Arg	gtc Val	aga Arg	aaa Lys	aat Asn 245	ggt Gly	gtt Val	gcc Ala	gcg Ala	cca Pro 250	tct Ser	gcc Ala	acc Thr	agc Ser	cag Gln 255	cta Leu	768
tca Ser	act Thr	cgc Arg	gcc Ala 260	ctg Leu	gaa Glu	Gl ^à aaa	Ile	ttt Phe 265	gaa Glu	gca Ala	act Thr	cat His	cga Arg 270	ttg Leu	att Ile	816

tac Tyr	ggo Gly	gct Ala 275	ггъ	g gat s Asp	gac Asp	tct Ser	ggt Gly 280	Gln	aga Arg	a tac g Tyr	ctg Leu	gcc Ala 285	Trp	tct Ser	gga Gly	864
Cac His	agt Ser 290	: Ата	cgt Arg	gtc y Val	gga Gly	gcc Ala 295	Ala	cga Arg	gat Asp	atg Met	gcc Ala 300	. Arg	gct Ala	gga	gtt Val	912
tca Ser 305	. TTE	ccg Pro	gag Glu	ato Ile	atg Met 310	caa Gln	gct Ala	ggt Gly	ggc	tgg Trp 315	Thr	aat Asn	gta Val	aat Asn	att Ile 320	960
gto Val	atg Met	aac Asn	tat Tyr	atc Ile 325	cgt Arg	aac Asn	ctg Leu	gat Asp	agt Ser 330	Glu	aca Thr	Gly aaa	gca Ala	atg Met 335	gtg Val	1008
cgc Arg	ctg Leu	ctg Leu	gaa Glu 340	Asp	Gly	gat Asp	ctc Leu	gag Glu 345	cca Pro	tct Ser	gct Ala	gga Gly	gac Asp 350	atg Met	aga Arg	1056
Ala	Ala	aac Asn 355	Leu	Trp	Pro	Ser	Pro 360	Leu	Met	Ile	Lys	Arg 365	Ser	Lys	Lys	1104
ASII	370	ctg Leu	АІА	ьeu	Ser	ьеи 375	Thr	Ala	Asp	Gln	Met 380	Val	Ser	Ala	Leu	1152
ьеи 385	Asp	gct Ala	Glu	Pro	90 390	Ile	Leu	Tyr	Ser	Glu 395	Tyr	Asp	Pro	Thr	Arg 400	1200
Pro	Pne	agt Ser	Glu	Ala 405	Ser	Met	Met	Gly	Leu 410	Leu	Thr	Asn	Leu	Ala 415	Asp	1248
Arg	Glu	ctg Leu	Val 420	His	Met	Ile	Asn	Trp 425	Ala	Lys	Arg	Val	Pro 430	Gly	Phe	1296
Val	Asp	ttg Leu 435	Thr	Leu	His	Asp	Gln 440	Val	His	Leu	Leu	Glu 445	Cys	Ala	Trp	1344
ьеu	450	atc Ile	Leu	Met	Ile	Gly 455	Leu	Val	Trp	Arg	Ser 460	Met	Glu	His	Pro	1392
465	ьys	cta Leu	Leu	Phe	A1a 470	Pro	Asn	Leu	Leu	Leu 475	Asp	Arg	Asn	Gln	Gly 480	1440
aaa Lys	tgt Cys	gta Val	gag Glu	ggc Gly 485	atg Met	gtg Val	gag Glu	Ile	ttc Phe 490	gac Asp	atg Met	ctg Leu	Leu	gct Ala 495	aca Thr	1488

tca Ser	tct Ser	cgg Arg	ttc Phe 500	Arg	atg Met	atg Met	aat Asn	ctg Leu 505	Gln	gga Gly	gag Glu	gag Glu	ttt Phe 510	gtg Val	tgc Cys	1536
ctc Leu	aaa Lys	tct Ser 515	att Ile	att Ile	ttg Leu	ctt Leu	aat Asn 520	tct Ser	gga Gly	gtg Val	tac Tyr	aca Thr 525	ttt Phe	ctg Leu	tcc Ser	1584
agc Ser	acc Thr 530	ctg Leu	aag Lys	tct Ser	ctg Leu	gaa Glu 535	gag Glu	aag Lys	gac Asp	cat His	atc Ile 540	cac His	cga Arg	gtc Val	ctg Leu	1632
gac Asp 545	aag Lys	atc Ile	aca Thr	gac Asp	act Thr 550	ttg Leu	atc Ile	cac His	ctg Leu	atg Met 555	gcc Ala	aag Lys	gca Ala	ggc Gly	ctg Leu 560	1680
acc Thr	ctg Leu	cag Gln	cag Gln	cag Gln 565	cac His	cag Gln	cgg Arg	ctg Leu	gcc Ala 570	cag Gln	ctc Leu	ctc Leu	ctc Leu	atc Ile 575	ctc Leu	1728
tcc Ser	cac His	atc Ile	agg Arg 580	cac His	atg Met	agt Ser	aac Asn	aaa Lys 585	ggc Gly	atg Met	gag Glu	cat His	ctg Leu 590	tac Tyr	agc Ser	1776
мес	ьуs	595	ГÀЗ	Asn	Val	Val	ccc Pro 600	Leu	Tyr	Asp	Leu	Leu 605	Leu	Glu	Ala	1824
АІА	610	Ala	His	Arg	Leu	His 615	gcg Ala	Pro	Thr	Ser	Arg 620	Gly	Gly	Ala	Ser	1872
Va1 625	GIu	Glu	Thr	Asp	Gln 630	Ser	cac His	Leu	Ala	Thr 635	Ala	Gly	Ser	Thr	Ser 640	1920
ser	HIS	ser	Leu	G1n 645	aag Lys	tat Tyr	tac Tyr	atc Ile	acg Thr 650	gly aaa	gag Glu	gca Ala	gag Glu	ggt Gly 655	ttc Phe	1968
cct Pro		Thr		tga												1983
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<223> Description of Artificial Sequence: Chimeric sequence Homosapiens-Bacteriophage P1

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135

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn 150

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu 170

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys 235

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu 245

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile 310 315

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg 345 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys 360 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu 375 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg 390 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 410 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 420 425 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp 440 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 455 Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly 475 470 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys 505 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 535 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545 550 555 Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser 585 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Ala Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser 615

<212> DNA

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<400> 14 atagcgccgg cgctgcagca caggagggtg ctatgag

37